

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/579,622
Source: IFWP
Date Processed by STIC: 5/26/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 05/26/2006

PATENT APPLICATION: US/10/579,622

TIME: 08:14:03

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05262006\J579622.raw

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5 <110> APPLICANT: Crusade Laboratories Limited
7     Sloane-Kettering Institute for Cancer Research
9     Brown, Susanne M
11    Dunn, Paul
13    Singh, Bhuvanesh
15    Ganly, Ian
19 <120> TITLE OF INVENTION: Mutant Viruses
23 <130> FILE REFERENCE: 6947-75757-01
C--> 27 <140> CURRENT APPLICATION NUMBER: US/10/579,622
C--> 27 <141> CURRENT FILING DATE: 2006-05-16
27 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/004908
29 <151> PRIOR FILING DATE: 2004-11-17
33 <150> PRIOR APPLICATION NUMBER: GB 0326798.6
35 <151> PRIOR FILING DATE: 2003-11-17
39 <150> PRIOR APPLICATION NUMBER: US 60/541,308
41 <151> PRIOR FILING DATE: 2004-02-03
45 <160> NUMBER OF SEQ ID NOS: 6
49 <170> SOFTWARE: PatentIn version 3.1
53 <210> SEQ ID NO: 1
55 <211> LENGTH: 918
57 <212> TYPE: DNA
59 <213> ORGANISM: Homo sapiens
63 <220> FEATURE:
65 <221> NAME/KEY: CDS
67 <222> LOCATION: (58)..(837)
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74 atg aac aag ttg aaa tca tcg cag aag gat aaa gtt cgt cag ttt atg      105
75 Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
76 1           5           10           15
78 atc ttc aca caa tct agt gaa aaa aca gca gta agt tgt ctt tct caa      153
79 Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
80           20           25           30
82 aat gac tgg aag tta gat gtt gca aca gat aat ttt ttc caa aat cct      201
83 Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
84           35           40           45
86 gaa ctt tat ata cga gag agt gta aaa gga tca ttg gac agg aag aag      249
87 Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
88           50           55           60
90 tta gaa cag ctg tac aat aga tac aaa gac cct caa gat gag aat aaa      297
91 Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys
92 65           70           75           80
94 att gga ata gat ggc ata cag cag ttc tgt gat gac ctg gca ctc gat      345

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95 Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp
96                               85                               90                               95
98 cca gcc agc att agt gtg ttg att att gca tgg aag ttc aga gca gca      393
99 Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala
100                               100                               105                               110
102 aca cag tgc gag ttc tcc aaa cag gag ttc atg gat ggc atg aca gaa      441
103 Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu
104                               115                               120                               125
106 tta gga tgt gac agc ata gaa aaa cta aag gcc cag ata ccc aag atg      489
107 Leu Gly Cys Asp Ser Ile Glu Lys Leu Lys Ala Gln Ile Pro Lys Met
108                               130                               135                               140
110 gaa caa gaa ttg aaa gaa cca gga cga ttt aag gat ttt tac cag ttt      537
111 Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe
112 145                               150                               155                               160
114 act ttt aat ttt gca aag aat cca gga caa aaa gga tta gat cta gaa      585
115 Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu
116                               165                               170                               175
118 atg gcc att gcc tac tgg aac tta gtg ctt aat gga aga ttt aaa ttc      633
119 Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Lys Phe
120                               180                               185                               190
122 tta gac tta tgg aat aaa ttt ttg ttg gaa cat cat aaa cga tca ata      681
123 Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile
124                               195                               200                               205
126 cca aaa gac act tgg aat ctt ctt tta gac ttc agt acg atg att gca      729
127 Pro Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser Thr Met Ile Ala
128                               210                               215                               220
130 gat gac atg tct aat tat gat gaa gaa gga gca tgg cct gtt ctt att      777
131 Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile
132 225                               230                               235                               240
134 gat gac ttt gtg gaa ttt gca cgc cct caa att gct ggg aca aaa agt      825
135 Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser
136                               245                               250                               255
138 aca aca gtg tag cactaaagga accttctaga atgtacatag tctgtacaat      877
139 Thr Thr Val
142 aaatacaaca gaaaattgca cagtcaattt ctgctggctg g      918
145 <210> SEQ ID NO: 2
147 <211> LENGTH: 259
149 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 2
157 Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
158 1                               5                               10                               15
161 Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
162                               20                               25                               30
165 Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
166                               35                               40                               45
169 Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
170                               50                               55                               60
173 Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys

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174 65          70          75          80
177 Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp
178          85          90          95
181 Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala
182          100          105          110
185 Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu
186          115          120          125
189 Leu Gly Cys Asp Ser Ile Glu Lys Leu Lys Ala Gln Ile Pro Lys Met
190          130          135          140
193 Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe
194 145          150          155          160
197 Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu
198          165          170          175
201 Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Lys Phe
202          180          185          190
205 Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile
206          195          200          205
209 Pro Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser Thr Met Ile Ala
210          210          215          220
213 Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile
214 225          230          235          240
217 Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser
218          245          250          255
221 Thr Thr Val
225 <210> SEQ ID NO: 3
227 <211> LENGTH: 876
229 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
235 <220> FEATURE:
237 <221> NAME/KEY: CDS
239 <222> LOCATION: (16)..(795)
243 <400> SEQUENCE: 3
244 ctggaggaca ccaac atg aac aag ttg aaa tca tcg cag aag gat aaa gtt      51
245          Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val
246          1          5          10
248 cgt cag ttt atg atc ttc aca caa tct agt gaa aaa aca gca gta agt      99
249 Arg Gln Phe Met Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser
250          15          20          25
252 tgt ctt tct caa aat gac tgg aag tta gat gtt gca aca gat aat ttt      147
253 Cys Leu Ser Gln Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe
254          30          35          40
256 ttc caa aat cct gaa ctt tat ata cga gag agt gta aaa gga tca ttg      195
257 Phe Gln Asn Pro Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu
258 45          50          55          60
260 gac agg aag aag tta gaa cag ctg tac aat aga tac aaa gac cct caa      243
261 Asp Arg Lys Lys Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln
262          65          70          75
264 gat gag aat aaa att gga ata gat ggc ata cag cag ttc tgt gat gac      291
265 Asp Glu Asn Lys Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp

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266      80      85      90
268 ctg gca ctc gat cca gcc agc att agt gtg ttg att att gcg tgg aag      339
269 Leu Ala Leu Asp Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys
270      95      100      105
272 ttc aga gca gca aca cag tgc gag ttc tcc aaa cag gag ttc atg gat      387
273 Phe Arg Ala Ala Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp
274      110      115      120
276 ggc atg aca gaa tta gga tgt gac agc aca gaa aaa cta aag gcc cag      435
277 Gly Met Thr Glu Leu Gly Cys Asp Ser Thr Glu Lys Leu Lys Ala Gln
278 125      130      135      140
280 ata ccc aag atg gaa caa gaa ttg aaa gaa cca gga cga ttt aag gat      483
281 Ile Pro Lys Met Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp
282      145      150      155
284 ttt tac cag ttt act ttt aat ttt gca aag aat cca gga caa aaa gga      531
285 Phe Tyr Gln Phe Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly
286      160      165      170
288 tta gat cta gaa atg gcc att gcc tac tgg aac tta gtg ctt aat gga      579
289 Leu Asp Leu Glu Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly
290      175      180      185
292 aga ttt aga ctc tta gac tta tgg aat aaa ttt ttg ttg gaa cat cat      627
293 Arg Phe Arg Leu Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His
294      190      195      200
296 aaa cga tca ata cca aaa gac act tgg aat ctt ctt tta gac ttc agt      675
297 Lys Arg Ser Ile Pro Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser
298 205      210      215      220
300 acg atg att gca gat gac atg tct aat tat gat gaa gaa gga gca tgg      723
301 Thr Met Ile Ala Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp
302      225      230      235
304 cct gtt ctt att gat gac ttt gtg gaa ttt gca cgc cct caa att gct      771
305 Pro Val Leu Ile Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala
306      240      245      250
308 ggg aca aaa agt aca aca gtg tag cactaaagga accttctaga atgtacatag      825
309 Gly Thr Lys Ser Thr Thr Val
310      255
312 tctgtacaat aaatacaaca gaaaattgca cagtcaattt ctgctggctg g      876
315 <210> SEQ ID NO: 4
317 <211> LENGTH: 259
319 <212> TYPE: PRT
321 <213> ORGANISM: Homo sapiens
325 <400> SEQUENCE: 4
327 Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
328 1      5      10      15
331 Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
332      20      25      30
335 Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
336      35      40      45
339 Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
340      50      55      60
343 Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys

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344 65          70          75          80
347 Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp
348          85          90          95
351 Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala
352          100          105          110
355 Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu
356          115          120          125
359 Leu Gly Cys Asp Ser Thr Glu Lys Leu Lys Ala Gln Ile Pro Lys Met
360          130          135          140
363 Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe
364 145          150          155          160
367 Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu
368          165          170          175
371 Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Arg Leu
372          180          185          190
375 Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile
376          195          200          205
379 Pro Lys Asp Thr Trp Asn Leu Leu Asp Phe Ser Thr Met Ile Ala
380          210          215          220
383 Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile
384 225          230          235          240
387 Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser
388          245          250          255
391 Thr Thr Val

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395 <210> SEQ ID NO: 5

397 <211> LENGTH: 64

399 <212> TYPE: DNA

401 <213> ORGANISM: Artificial sequence

405 <220> FEATURE:

407 <223> OTHER INFORMATION: DNA nucleotide sequence encoding the siRNA construct
designed to

408 target expression of the SCCRO gene

410 <400> SEQUENCE: 5

411 gatccccgtt cagagcagca acacagttca agagactgtg ttgctgctct gaactttttg 60

413 gaaa 64

416 <210> SEQ ID NO: 6

418 <211> LENGTH: 60

420 <212> TYPE: DNA

422 <213> ORGANISM: Artificial sequence

426 <220> FEATURE:

428 <223> OTHER INFORMATION: Nucleotide sequence encoding control siRNA

430 <400> SEQUENCE: 6

431 gatccccctg ctacctacac tccctcttca agagagaggg agtgtaggta gacgttttta 60

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/579,622

DATE: 05/26/2006

TIME: 08:14:04

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Output Set: N:\CRF4\05262006\J579622.raw

L:27 M:270 C: Current Application Number differs, Replaced Current Application No

L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date